

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/757,041

DATE: 03/22/2001
TIME: 23:59:51

INPUT SET: S36561.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Reed, John C.
6 Sato, Takaaki
7
8 (ii) TITLE OF INVENTION: CD40 Associated Proteins
9
10 (iii) NUMBER OF SEQUENCES: 17
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Campbell and Flores
14 (B) STREET: 4370 La Jolla Village Drive, Suite 700
15 (C) CITY: San Diego
16 (D) STATE: California
17 (E) COUNTRY: USA
18 (F) ZIP: 92122
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: 09/757,041
28 (B) FILING DATE:
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: 08/349,357
33 (B) FILING DATE:
34
35
36
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Campbell, Cathryn A.
39 (B) REGISTRATION NUMBER: 31,815
40 (C) REFERENCE/DOCKET NUMBER: P-LJ 1203
41
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: (619) 535-9001
44 (B) TELEFAX: (619) 535-8949
45
46

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47 (2) INFORMATION FOR SEQ ID NO:1:
48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 2240 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear
5455
56 (ix) FEATURE:

57 (A) NAME/KEY: CDS

58 (B) LOCATION: 137..1766
5960
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62

63	AGAAGTGATG CCACTTGGTT AAGGTCCCAG AGCAGGTCAG AATCAGACCT AGGATCAGAA	60
64		
65	ACCTGGCTCC TGGCTCCTGG CTCCTACTC TTCTAAGGAT CGCTGTCCTG ACAGAAGAGA	120
66		
67	ACTCCTCTTT CCTAAA ATG GAG TCG AGT AAA AAG ATG GAC TCT CCT GGC	169
68	Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly	
69	1 5 10	
70		
71	GCG CTG CAG ACT AAC CCG CCG CTA AAG CTG CAC ACT GAC CGC AGT GCT	217
72	Ala Leu Gln Thr Asn Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala	
73	15 20 25	
74		
75	GGG ACG CCA GTT TTT GTC CCT GAA CAA GGA GGT TAC AAG GAA AAG TTT	265
76	Gly Thr Pro Val Phe Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe	
77	30 35 40	
78		
79	GTG AAG ACC GTG GAG GAC AAG TAC AAG TGT GAG AAG TGC CAC CTG GTG	313
80	Val Lys Thr Val Glu Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val	
81	45 50 55	
82		
83	CTG TGC AGC CCG AAG CAG ACC GAG TGT GGG CAC CGC TCC TGC GAG AGC	361
84	Leu Cys Ser Pro Lys Gln Thr Glu Cys Gly His Arg Ser Cys Glu Ser	
85	60 65 70 75	
86		
87	TGC ATG GCG GCC CTG CTG AGC TCT TCA AGT CCA AAA TGT ACA GCG TGT	409
88	Cys Met Ala Ala Leu Leu Ser Ser Ser Pro Lys Cys Thr Ala Cys	
89	80 85 90	
90		
91	CAA GAG AGC ATC GTT AAA GAT AAG GTG TTT AAG GAT AAT TGC TGC AAG	457
92	Gln Glu Ser Ile Val Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys	
93	95 100 105	
94		
95	AGA GAA ATT CTG GCT CTT CAG ATC TAT TGT CGG AAT GAA AGC AGA GGT	505
96	Arg Glu Ile Leu Ala Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly	
97	110 115 120	
98		
99	TGT GCA GAG CAG TTA ACG CTG GGA CAT CTG CTG GTG CAT TTA AAA AAT	553

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100	Cys	Ala	Glu	Gln	Leu	Thr	Leu	Gly	His	Leu	Leu	Val	His	Leu	Lys	Asn	
101		125					130					135					
102																	
103	GAT	TGC	CAT	TTT	GAA	GAA	CTT	CCA	TGT	GTG	CGT	CCT	GAC	TGC	AAA	GAA	601
104	Asp	Cys	His	Phe	Glu	Glu	Leu	Pro	Cys	Val	Arg	Pro	Asp	Cys	Lys	Glu	
105	140					145					150					155	
106																	
107	AAG	GTC	TTG	AGG	AAA	GAC	CTG	CGA	GAC	CAC	GTG	GAG	AAG	GCG	TGT	AAA	649
108	Lys	Val	Leu	Arg	Lys	Asp	Leu	Arg	Asp	His	Val	Glu	Lys	Ala	Cys	Lys	
109					160				165						170		
110																	
111	TAC	CGG	GAA	GCC	ACA	TGC	AGC	CAC	TGC	AAG	AGT	CAG	GTT	CCG	ATG	ATC	697
112	Tyr	Arg	Glu	Ala	Thr	Cys	Ser	His	Cys	Lys	Ser	Gln	Val	Pro	Met	Ile	
113				175					180					185			
114																	
115	GCG	CTG	CAG	AAA	CAC	GAA	GAC	ACC	GAC	TGT	CCC	TGC	GTG	GTG	GTG	TCC	745
116	Ala	Leu	Gln	Lys	His	Glu	Asp	Thr	Asp	Cys	Pro	Cys	Val	Val	Val	Ser	
117			190					195					200				
118																	
119	TGC	CCT	CAC	AAG	TGC	AGC	GTC	CAG	ACT	CTC	CTG	AGG	AGC	GAG	GGG	ACA	793
120	Cys	Pro	His	Lys	Cys	Ser	Val	Gln	Thr	Leu	Leu	Arg	Ser	Glu	Gly	Thr	
121		205					210					215					
122																	
123	AAC	CAG	CAG	ATC	AAG	GCC	CAC	GAG	GCC	AGC	TCC	GCC	GTG	CAG	CAC	GTC	841
124	Asn	Gln	Gln	Ile	Lys	Ala	His	Glu	Ala	Ser	Ser	Ala	Val	Gln	His	Val	
125	220					225					230					235	
126																	
127	AAC	CTG	CTG	AAG	GAG	TGG	AGC	AAC	TCG	CTC	GAA	AAG	AAG	GTT	TCC	TTG	889
128	Asn	Leu	Leu	Lys	Glu	Trp	Ser	Asn	Ser	Leu	Glu	Lys	Lys	Val	Ser	Leu	
129					240					245					250		
130																	
131	TTG	CAG	AAT	GAA	AGT	GTA	GAA	AAA	AAC	AAG	AGC	ATA	CAA	AGT	TTG	CAC	937
132	Leu	Gln	Asn	Glu	Ser	Val	Glu	Lys	Asn	Lys	Ser	Ile	Gln	Ser	Leu	His	
133				255					260					265			
134																	
135	AAT	CAG	ATA	TGT	AGC	TTT	GAA	ATT	GAA	ATT	GAG	AGA	CAA	AAG	GAA	ATG	985
136	Asn	Gln	Ile	Cys	Ser	Phe	Glu	Ile	Glu	Ile	Glu	Arg	Gln	Lys	Glu	Met	
137			270					275					280				
138																	
139	CTT	CGA	AAT	AAT	GAA	TCC	AAA	ATC	CTT	CAT	TTA	CAG	CGA	GTG	ATA	GAC	1033
140	Leu	Arg	Asn	Asn	Glu	Ser	Lys	Ile	Leu	His	Leu	Gln	Arg	Val	Ile	Asp	
141		285					290					295					
142																	
143	AGC	CAA	GCA	GAG	AAA	CTG	AAG	GAG	CTT	GAC	AAG	GAG	ATC	CGG	TCC	TTC	1081
144	Ser	Gln	Ala	Glu	Lys	Leu	Lys	Glu	Leu	Asp	Lys	Glu	Ile	Arg	Ser	Phe	
145	300					305					310					315	
146																	
147	CGG	CAG	AAC	TGG	GAG	GAA	GCA	GAC	AGC	ATG	AAG	AGC	AGC	GTG	GAG	TCC	1129
148	Arg	Gln	Asn	Trp	Glu	Glu	Ala	Asp	Ser	Met	Lys	Ser	Ser	Val	Glu	Ser	
149					320					325					330		
150																	
151	CTC	CAG	AAC	CGC	GTG	ACC	GAG	CTG	GAG	AGC	GTG	GAC	AAG	AGC	GCG	GGG	1177
152	Leu	Gln	Asn	Arg	Val	Thr	Glu	Leu	Glu	Ser	Val	Asp	Lys	Ser	Ala	Gly	

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	335	340	345	
153				
154				
155	CAA GTG GCT CGG AAC ACA GGC CTG CTG GAG TCC CAG CTG AGC CGG CAT			1225
156	Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His			
157	350	355	360	
158				
159	GAC CAG ATG CTG AGT GTG CAC GAC ATC CGC CTA GCC GAC ATG GAC CTG			1273
160	Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala Asp Met Asp Leu			
161	365	370	375	
162				
163	CGC TTC CAG GTC CTG GAG ACC GCC AGC TAC AAT GGA GTG CTC ATC TGG			1321
164	Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp			
165	380	385	390	395
166				
167	AAG ATT CGC GAC TAC AAG CGG CGG AAG CAG GAG GCC GTC ATG GGG AAG			1369
168	Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys			
169	400	405	410	
170				
171	ACC CTG TCC CTT TAC AGC CAG CCT TTC TAC ACT GGT TAC TTT GGC TAT			1417
172	Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr			
173	415	420	425	
174				
175	AAG ATG TGT GCC AGG GTC TAC CTG AAC GGG GAC GGG ATG GGG AAG GGG			1465
176	Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly			
177	430	435	440	
178				
179	ACG CAC TTG TCG CTG TTT TTT GTC ATC ATG CGT GGA GAA TAT GAT GCC			1513
180	Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala			
181	445	450	455	
182				
183	CTG CTT CCT TGG CCG TTT AAG CAG AAA GTG ACA CTC ATG CTG ATG GAT			1561
184	Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp			
185	460	465	470	475
186				
187	CAG GGG TCC TCT CGA CGT CAT TTG GGA GAT GCA TTC AAG CCC GAC CCC			1609
188	Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro			
189	480	485	490	
190				
191	AAC AGC AGC AGC TTC AAG AAG CCC ACT GGA GAG ATG AAT ATC GCC TCT			1657
192	Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser			
193	495	500	505	
194				
195	GGC TGC CCA GTC TTT GTG GCC CAA ACT GTT CTA GAA AAT GGG ACA TAT			1705
196	Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr			
197	510	515	520	
198				
199	ATT AAA GAT GAT ACA ATT TTT ATT AAA GTC ATA GTG GAT ACT TCG GAT			1753
200	Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp			
201	525	530	535	
202				
203	CTG CCC GAT CCC T GATAAGTAGC TGGGGAGGTG GATTTAGCAG AAGGCAACTC			1806
204	Leu Pro Asp Pro			
205	540			

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206
207 CTCTGGGGGA TTTGAACCGG TCTGTCTTCA CTGAGGTCCT CGCGCTCAGA AAAGGACCTT 1866
208
209 GTGAGACGGA GGAAGCGGCA GAAGGCGGAC GCGTGCCGGC GGGAGGAGCC ACGCGTGAGA 1926
210
211 CACCTGACAC GTTTTATAAT AGACTAGCCA CACTTCACTC TGAAGAATTA TTTATCCTTC 1986
212
213 AACAAGCATA AATATTGCTG TCAGAGAAGG TTTTCATTTT CATTTTAAA GATCTAGTTA 2046
214
215 ATTAAGGTGG AAAACATATA TGCTAAACAA AAGAAACATG ATTTTCTTC CTAAACTTG 2106
216
217 AACACCAAAA AACACACACA CACACACACA CGTGGGGATA GCTGGACATG TCAGCATGTT 2166
218
219 AAGTAAAGG AGAATTTATG AAATAGTAAT GCAATTCTGA TATCTTCTTT CTAAAATTCA 2226
220
221 AGAGTGCAAT TTTG 2240
222
223

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

234
235 Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
236 1 5 10 15
237
238 Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
239 20 25 30
240
241 Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
242 35 40 45
243
244 Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
245 50 55 60
246
247 Gln Thr Glu Cys Gly His Arg Ser Cys Glu Ser Cys Met Ala Ala Leu
248 65 70 75 80
249
250 Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
251 85 90 95
252
253 Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
254 100 105 110
255
256 Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
257 115 120 125
258

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SEQUENCE VERIFICATION REPORT
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Line

Error

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